

#12

AU 1644

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/522,752
 DATE: 10/11/2000
 TIME: 10:58:23

Input Set : A:\1855.1064003.TXT
 Output Set: N:\CRF3\10112000\I522752.raw

4 <110> APPLICANT: Andrew, David P.
 5 Zabel, Brian A.
 6 Ponath, Paul D.
 8 <120> TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
 9 IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
 12 <130> FILE REFERENCE: 1855.1064-003
 14 <140> CURRENT APPLICATION NUMBER: US 09/522,752
 C--> 15 <141> CURRENT FILING DATE: 2000-05-10
 17 <150> PRIOR APPLICATION NUMBER: US 09/266,464
 18 <151> PRIOR FILING DATE: 1999-03-11
 20 <160> NUMBER OF SEQ ID NOS: 15
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2577
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (58)...(1131)
 33 <400> SEQUENCE: 1
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 35 Met
 36 1
 38 gct gat gac tat ggc tct gaa tcc aca tct tcc atg gaa gac tac gtt 108
 39 Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Met Glu Asp Tyr Val
 40 5 10 15
 42 aac ttc aac ttc act gac ttc tac tgt gag aaa aac aat gtc agg cag 156
 43 Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln
 44 20 25 30
 46 ttt gcg agc cat ttc ctc cca ccc ttg tac tgg ctc gtg ttc atc gtg 204
 47 Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val
 48 35 40 45
 50 ggt gcc ttg ggc aac agt ctt gtt atc ctt gtc tac tgg tac tgc aca 252
 51 Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr
 52 50 55 60 65
 54 aga gtg aag acc atg acc gac atg ttc ctt ttg aat ttg gca att gct 300
 55 Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala
 56 70 75 80
 58 gac ctc ctc ttt ctt gtc act ctt ccc ttc tgg gcc att gct gct gct 348
 59 Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala
 60 85 90 95
 62 gac cag tgg aag ttc cag acc ttc atg tgc aag gtg gtc aac agc atg 396
 63 Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met
 64 100 105 110
 66 tac aag atg aac ttc tac agc tgt gtg ttg ctg atc atg tgc atc agc 444
 67 Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser
 68 115 120 125

ENTERED

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70 gtg gac agg tac att gcc att gcc cag gcc atg aga gca cat act tgg      492
71 Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp
72 130                               135                               140                               145
74 agg gag aaa agg ctt ttg tac agc aaa atg gtt tgc ttt acc atc tgg      540
75 Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp
76                               150                               155                               160
78 gta ttg gca gct gct ctc tgc atc cca gaa atc tta tac agc caa atc      588
79 Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile
80                               165                               170                               175
82 aag gag gaa tcc ggc att gct atc tgc acc atg gtt tac cct agc gat      636
83 Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp
84                               180                               185                               190
86 gag agc acc aaa ctg aag tca gct gtc ttg acc ctg aag gtc att ctg      684
87 Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu
88                               195                               200                               205
90 ggg ttc ttc ctt ccc ttc gtg gtc atg gct tgc tgc tat acc atc atc      732
91 Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile
92 210                               215                               220                               225
94 att cac acc ctg ata caa gcc aag aag tct tcc aag cac aaa gcc cta      780
95 Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu
96                               230                               235                               240
98 aaa gtg acc atc act gtc ctg acc gtc ttt gtc ttg tct cag ttt ccc      828
99 Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro
100                               245                               250                               255
102 tac aac tgc att ttg ttg gtg cag acc att gac gcc tat gcc atg ttc      876
103 Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe
104                               260                               265                               270
106 atc tcc aac tgt gcc gtt tcc acc aac att gac atc tgc ttc cag gtc      924
107 Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val
108                               275                               280                               285
110 acc cag acc atc gcc ttc ttc cac agt tgc ctg aac cct gtt ctc tat      972
111 Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr
112 290                               295                               300                               305
114 gtt ttt gtg ggt gag aga ttc cgc cgg gat ctc gtg aaa acc ctg aag      1020
115 Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys
116                               310                               315                               320
118 aac ttg ggt tgc atc agc cag gcc cag tgg gtt tca ttt aca agg aga      1068
119 Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg
120                               325                               330                               335
122 gag gga agc ttg aag ctg tgc tct atg ttg ctg gag aca acc tca gga      1116
123 Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly
124                               340                               345                               350
126 gca ctc tcc ctc tga ggggtcttct ctgaggtgca tggttctttt ggaagaaatg      1171
127 Ala Leu Ser Leu *
128                               355
130 agaaatacat gaaacagttt cccactgat gggaccagag agagtgaag agaaaagaaa      1231
131 actcagaaag ggatgaatct gaactatatg attacttgta gtcagaattt gccaaagcaa      1291
132 atatttcaa atcaactgac tagtgcagga ggctgttgat tggctcttga ctgtgatgcc      1351
133 cgcaattctc aaaggaggac taaggaccgg cactgtggag caccctggct ttgccactcg      1411

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134 ccggagcadc aatgccgctg cctctggagg agcccttggg tttctccat gcactgtgaa 1471
135 cttctgtggc ttcagttctc atgctgcctc ttccaaaagg ggacacagaa gcactggctg 1531
136 ctgctacaga ccgcaaaagg agaaagtctc gtgaaaatgt ccatcttttg gaaattttct 1591
137 accctgctct tgagcctgat aacctatgcc aggtcttata gattcctgat ctagaacctt 1651
138 tccaggcaat ctcagacctc atttcttctt gttctccttg tctgtttctg ggccagttaa 1711
139 ggtccttggt ctgattttga aacgatctgc aggtcttgcc agtgaacccc tggacaactg 1771
140 accacaccca caaggcatcc aaagtctgtt ggcttccaat ccattttctg gtctgctggg 1831
141 aggttttaac ctagacaagg attccgctta ttccttggtg tggtagacagt gtctctccat 1891
142 ggctgagca gggagattat aacagctggg ttcgcaggag ccagccttgg ccctgttgta 1951
143 ggcttggtct gttgagtgcc acttgctttg ggtccaccgt ctgtctgctc cctagaaaaa 2011
144 ggctggttct ttttggccct cttctttctg agggccactt tattctgagg aatacagtga 2071
145 gcagatatgg gcagcagcca ggtagggcaa aggggtgaag cgcaggcctt gctggaaggc 2131
146 tatttacttc catgcttctc ctttctttac tctatagtgg caacatttta aaagctttta 2191
147 acttagagat taggctgaaa aaaataagta atggaattca cctttgcacg tttgtgtct 2251
148 tttctatcat gatttggcaa aatgcatcac ctttggaaat atttcacata ttggaaaagt 2311
149 gctttttaat gtgtatatga agcattaatt acttgctcact ttctttaccg tgtctcaata 2371
150 ttttaagtgt gtgcaattaa agatcaataa gatacattaa gagtgtgaag gctgggtctga 2431
151 aggtagttag ctatctcaat cggattgttc acactcagtt acagattgaa ctccttggtc 2491
152 tacttccctg cttctctcta ctgcaattga ctagctttta aaaaaaagtg tgaagagtaa 2551
153 gcaataggga taaggaaata agatct 2577
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 357
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 2
161 Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
162 1 5 10 15
163 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
164 20 25 30
165 Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
166 35 40 45
167 Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
168 50 55 60
169 Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Asn Leu Ala Ile
170 65 70 75 80
171 Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
172 85 90 95
173 Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
174 100 105 110
175 Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
176 115 120 125
177 Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
178 130 135 140
179 Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
180 145 150 155 160
181 Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln
182 165 170 175
183 Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
184 180 185 190

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185 Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
186      195      200      205
187 Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
188      210      215      220
189 Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
190 225      230      235      240
191 Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
192      245      250      255
193 Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
194      260      265      270
195 Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
196      275      280      285
197 Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
198      290      295      300
199 Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
200 305      310      315      320
201 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
202      325      330      335
203 Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
204      340      345      350
205 Gly Ala Leu Ser Leu
206      355
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 26
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
217 <400> SEQUENCE: 3
218 Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
219 1      5      10      15
220 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys
221      20      25
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 35
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Oligonucleotide primer
233 <400> SEQUENCE: 4
234 tcgaagggat ccctaacatg gctgatgact atggc
236 <210> SEQ ID NO: 5
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Oligonucleotide primer
246 <400> SEQUENCE: 5
247 aagaagtcta gaaccctca gagggagagt gctcc

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35

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Input Set : A:\1855.1064003.TXT
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249 <210> SEQ ID NO: 6
250 <211> LENGTH: 30
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Oligonucleotide primer
259 <400> SEQUENCE: 6
260 tcgaagaagc ttatgaacct gtggctcctg
262 <210> SEQ ID NO: 7
263 <211> LENGTH: 30
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Oligonucleotide primer
272 <400> SEQUENCE: 7
273 aagaagtcta gatcacagtc ctgaattagc
275 <210> SEQ ID NO: 8
276 <211> LENGTH: 879
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <400> SEQUENCE: 8
281 atgaacctgt ggtccttggc ctgcctgggtg gccggcttcc tgggagcctg ggcctccgct
282 gtccacaccc aaggtgtctt tgaggactgc tgcctggcct accactaccc cattgggtgg
283 gctgtgtctc gccgcgctg gacttaccgg atccaggagg tgagcgggag ctgcaatctg
284 cctgtctcga tattctacct cccaagaga cacaggaagg tgtgtgggaa ccccaaaagc
285 agggaggtgc agagagccat gaagctcctg gatgctcgaa ataaggtttt tgcaaagctc
286 caccacaaca ygcagacctt ccaagcaggc cctcatgctg taaagaagtt gatttctgga
287 aactccaagt tatcatcatc caagtttagc aatcccatca gcagcagcaa gaggaatgac
288 tccctcctga tatcagctaa ttcaggactg tgagccggct catttctggg ctccatcggc
289 acaggagggg ccggatcttt ctccgataaa accgtcgccc tacagaccca gctgtcccca
290 cgctctgtgc ttttgggtca agtcttaatc cctgcacctg agttggtcct cctctgtcac
291 ccccaaccac tcttgcctgt ctggcaactg gaaagaagga gttggcctga ttttaacctt
292 ttgccgtctc ggggaacagc acaatcctgg gcagccagtg gctctttagt agaaaactta
293 ggatacctct ctcaatttct gttcttggcc gtccaccccg ggccatgccg gtgtgtcctc
294 tgggtccctt ccaaaaatct ggtcattcaa ggatccctc ccaaggctat gcttttctat
295 aacttttaaa taaaccttgg ggggtgaatg gaataaaaa
297 <210> SEQ ID NO: 9
298 <211> LENGTH: 150
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo Sapiens
302 <220> FEATURE:
303 <221> NAME/KEY: VARIANT
304 <222> LOCATION: (104)...(104)
305 <223> OTHER INFORMATION: Xaa= Met or Thr
307 <400> SEQUENCE: 9
308 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
309 1 5 10 15
310 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
311 20 25 30

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FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/522,752

DATE: 10/11/2000
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Input Set : A:\1855.1064003.TXT
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11